

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: Fri Jul 13 08:23:43 EDT 2007

=====

Application No: 10576281 Version No: 2.1

Input Set:

Output Set:

Started: 2007-07-13 08:23:22.883
Finished: 2007-07-13 08:23:23.171
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 288 ms
Total Warnings: 1
Total Errors: 0
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> Toshihiro NAKAJIMA
Tetsuya AMANO
Lei ZHANG
Rie IKEDA
Satoshi YAMASAKI
Naoko YAGISHITA

<120> Method of inhibiting secretase activity

<130> L7350.0007

<140> 10576281

<141> 2007-07-06

<150> PCT/JP2004/015950

<151> 2004-10-20

<150> JP2003-359704

<151> 2003-10-20

<160> 21

<170> PatentIn version 3.4

<210> 1

<211> 3374

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (403)..(2256)

<400> 1

gccctttctt atgagcatgc ctgtgttggg ttgacagtga gggtaataat gacttgttgg 60

ttgattgtag atatagggct ctcccttgca aggtaattag gctccttaa ttacctgtaa 120

gattttcttg ccacagcatc cattctggtt aggetggtga tcttctgagt agtgatagat 180

tggttggtgg tgaggtttac aggtgttccc ttctcttact cctggtgttg gctacaatca 240

ggtggcgtct agagcagcat gggacaggtg ggtaagggga gtcttctcat tatgcagaag 300

tgatcaactt aaatctctgt cagatctacc tttatgtagc ccggcagtcg cgcggattga 360

gcgggctcgc ggcgctgggt tcctggtctc cgggccaggg ca atg ttc cgc acg 414

Met Phe Arg Thr

1

gca gtg atg atg gcg gcc agc ctg gcg ctg acc ggg gct gtg gtg gct 462

Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly Ala Val Val Ala

5

10

15

20

cac gcc tac tac ctc aaa cac cag ttc tac ccc act gtg gtg tac ctg	510
His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr Val Val Tyr Leu	
25 30 35	
acc aag tcc agc ccc agc atg gca gtc ctg tac atc cag gcc ttt gtc	558
Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile Gln Ala Phe Val	
40 45 50	
ctt gtc ttc ctt ctg ggc aag gtg atg ggc aag gtg ttc ttt ggg caa	606
Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val Phe Phe Gly Gln	
55 60 65	
ctg agg gca gca gag atg gag cac ctt ctg gaa cgt tcc tgg tac gcc	654
Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg Ser Trp Tyr Ala	
70 75 80	
gtc aca gag act tgt ctg gcc ttc acc gtt ttt cgg gat gac ttc agc	702
Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg Asp Asp Phe Ser	
85 90 95 100	
ccc cgc ttt gtt gca ctc ttc act ctt ctt ctc ttc ctc aaa tgt ttc	750
Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Leu Phe Leu Lys Cys Phe	
105 110 115	
cac tgg ctg gct gag gac cgt gtg gac ttt atg gaa cgc agc ccc aac	798
His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu Arg Ser Pro Asn	
120 125 130	
atc tcc tgg ctc ttt cac tgc cgc att gtc tct ctt atg ttc ctc ctg	846
Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu Met Phe Leu Leu	
135 140 145	
ggc atc ctg gac ttc ctc ttc gtc agc cac gcc tat cac agc atc ctg	894
Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr His Ser Ile Leu	
150 155 160	
acc cgt ggg gcc tct gtg cag ctg gtg ttt ggc ttt gag tat gcc atc	942
Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe Glu Tyr Ala Ile	
165 170 175 180	
ctg atg acg atg gtg ctc acc atc ttc atc aag tat gtg ctg cac tcc	990
Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr Val Leu His Ser	
185 190 195	
gtg gac ctc cag agt gag aac ccc tgg gac aac aag gct gtg tac atg	1038
Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys Ala Val Tyr Met	
200 205 210	
ctc tac aca gag ctg ttt aca ggc ttc atc aag gtt ctg ctg tac atg	1086
Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val Leu Leu Tyr Met	
215 220 225	
gcc ttc atg acc atc atg atc aag gtg cac acc ttc cca ctc ttt gcc	1134
Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe Pro Leu Phe Ala	
230 235 240	
atc cgg ccc atg tac ctg gcc atg aga cag ttc aag aaa gct gtg aca	1182

Ile	Arg	Pro	Met	Tyr	Leu	Ala	Met	Arg	Gln	Phe	Lys	Lys	Ala	Val	Thr				
245					250					255					260				
gat	gcc	atc	atg	tct	cgc	cga	gcc	atc	cgc	aac	atg	aac	acc	ctg	tat	1230			
Asp	Ala	Ile	Met	Ser	Arg	Arg	Ala	Ile	Arg	Asn	Met	Asn	Thr	Leu	Tyr				
265					270					275									
cca	gat	gcc	acc	cca	gag	gag	ctc	cag	gca	atg	gac	aat	gtc	tgc	atc	1278			
Pro	Asp	Ala	Thr	Pro	Glu	Glu	Leu	Gln	Ala	Met	Asp	Asn	Val	Cys	Ile				
280					285					290									
atc	tgc	cga	gaa	gag	atg	gtg	act	ggc	gcc	aag	aga	ctg	ccc	tgc	aac	1326			
Ile	Cys	Arg	Glu	Glu	Met	Val	Thr	Gly	Ala	Lys	Arg	Leu	Pro	Cys	Asn				
295					300					305									
cac	att	ttc	cat	acc	agc	tgc	ctg	cgc	tcc	tgg	ttc	cag	cgg	cag	cag	1374			
His	Ile	Phe	His	Thr	Ser	Cys	Leu	Arg	Ser	Trp	Phe	Gln	Arg	Gln	Gln				
310					315					320									
acc	tgc	ccc	acc	tgc	cgt	atg	gat	gtc	ctt	cgt	gca	tgc	ctg	cca	gcg	1422			
Thr	Cys	Pro	Thr	Cys	Arg	Met	Asp	Val	Leu	Arg	Ala	Ser	Leu	Pro	Ala				
325					330					335					340				
cag	tca	cca	cca	ccc	ccg	gag	cct	gcg	gat	cag	ggg	cca	ccc	cct	gcc	1470			
Gln	Ser	Pro	Pro	Pro	Pro	Glu	Pro	Ala	Asp	Gln	Gly	Pro	Pro	Pro	Ala				
345					350					355									
ccc	cac	ccc	cca	cca	ctc	ttg	cct	cag	ccc	ccc	aac	ttc	ccc	cag	ggc	1518			
Pro	His	Pro	Pro	Pro	Leu	Leu	Pro	Gln	Pro	Pro	Asn	Phe	Pro	Gln	Gly				
360					365					370									
ctc	ctg	cct	cct	ttt	cct	cca	ggc	atg	ttc	cca	ctg	tgg	ccc	ccc	atg	1566			
Leu	Leu	Pro	Pro	Phe	Pro	Pro	Gly	Met	Phe	Pro	Leu	Trp	Pro	Pro	Met				
375					380					385									
ggc	ccc	ttt	cca	cct	gtc	ccg	cct	ccc	ccc	agc	tca	gga	gag	gct	gtg	1614			
Gly	Pro	Phe	Pro	Pro	Val	Pro	Pro	Pro	Pro	Ser	Ser	Gly	Glu	Ala	Val				
390					395					400									
gct	cct	cca	tcc	acc	agt	gca	gca	gcc	ctt	tct	cgg	ccc	agt	gga	gca	1662			
Ala	Pro	Pro	Ser	Thr	Ser	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Ser	Gly	Ala				
405					410					415					420				
gct	aca	acc	aca	gct	gct	ggc	acc	agt	gct	act	gct	gct	tct	gcc	aca	1710			
Ala	Thr	Thr	Thr	Ala	Ala	Gly	Thr	Ser	Ala	Thr	Ala	Ala	Ser	Ala	Thr				
425					430					435									
gca	tct	ggc	cca	ggc	tct	ggc	tct	gcc	cca	gag	gct	ggc	cct	gcc	cct	1758			
Ala	Ser	Gly	Pro	Gly	Ser	Gly	Ser	Ala	Pro	Glu	Ala	Gly	Pro	Ala	Pro				
440					445					450									
ggc	ttc	ccc	ttc	cct	cct	ccc	tgg	atg	ggc	atg	ccc	ctg	cct	cca	ccc	1806			
Gly	Phe	Pro	Phe	Pro	Pro	Pro	Trp	Met	Gly	Met	Pro	Leu	Pro	Pro	Pro				
455					460					465									
ttt	gcc	ttc	ccc	cca	atg	cct	gtg	ccc	cct	gcg	ggc	ttt	gct	ggg	ctg	1854			
Phe	Ala	Phe	Pro	Pro	Met	Pro	Val	Pro	Pro	Ala	Gly	Phe	Ala	Gly	Leu				

470	475	480	
acc cca gag gag cta cga gct ctg gag ggc cat gag cgg cag cac ctg			1902
Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu Arg Gln His Leu			
485	490	495	500
gag gcc cgg ctg cag agc ctg cgt aac atc cac aca ctg ctg gac gcc			1950
Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr Leu Leu Asp Ala			
505	510	515	
gcc atg ctg cag atc aac cag tac ctc acc gtg ctg gcc tcc ttg ggg			1998
Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu Ala Ser Leu Gly			
520	525	530	
ccc ccc cgg cct gcc act tca gtc aac tcc act gag ggg act gcc act			2046
Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu Gly Thr Ala Thr			
535	540	545	
aca gtt gtt gct gct gcc tcc tcc acc agc atc cct agc tca gag gcc			2094
Thr Val Val Ala Ala Ala Ser Ser Thr Ser Ile Pro Ser Ser Glu Ala			
550	555	560	
acg acc cca acc cca gga gcc tcc cca cca gcc cct gaa atg gaa agg			2142
Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro Glu Met Glu Arg			
565	570	575	580
cct cca gct cct gag tca gtg ggc aca gag gag atg cct gag gat gga			2190
Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met Pro Glu Asp Gly			
585	590	595	
gag ccc gat gca gca gag ctc cgc cgg cgc cgc ctg cag aag ctg gag			2238
Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu Gln Lys Leu Glu			
600	605	610	
tct cct gtt gcc cac tga cactgcccc gcccagcccc agcctctgct			2286
Ser Pro Val Ala His			
615			
cttttgagca gccctcgctg gaacatgtcc tgccaccaag tgccagctcc ctctctgtct			2346
gcaccaggga gtagtaccac cagctctgag aaagaggcgg catcccctag gccaaagtga			2406
aagaggctgg gggtccatt tgactccagt ccagggcagc catggggatc tcgggtcagt			2466
tccagccttc ctctccaaact cttcagccct gtgttctgct ggggccatga aggcagaagg			2526
tttagcctct gagaagccct cttcttcccc caccctttc caggagaagg ggctgccct			2586
ccaagcccta cttgtatgtg cggagtcaca ctgcagtgcc gaacagtatt agctcccgtt			2646
cccaagtgtg gactccagag gggetggagg caagctatga acttgetcgc tggcccaccc			2706
ctaagactgg taccatttc cttttcttac cctgatctcc ccagaagcct cttgtggtgg			2766
tggetgtgcc ccctatgcc tgtggcattt ctgcgtctta ctggcaacca cacaactcag			2826
ggaaaggaat gcctgggagt gggggtgcag gcgggcagca ctgagggacc ctgccccgcc			2886

```

cctcccccca ggcccccttc ccctgcagct tctcaagtga gactgacctg tctcaccag 2946
cagccactgc ccagccgcac tccaggcaag ggccagtgcg cctgctcctg accactgcaa 3006
tcccagcgcc caaggaaggc cactttctcaa ctggcagaac ttctgaagtt tagaattgga 3066
attacttcct tactagtgtc ttttggctta aattttgtct tttgaagttg aatgcttaat 3126
cccgggaaaag aggaacagga gtgccagact cctgggtcttt ccagtttaga aaaggctctg 3186
tgccaaggag ggaccacagg agctgggacc tgctgcccc tgccttttcc ccttggtttt 3246
gtgttacaag agttgttgga gacagtttca gatgattatt taatttgtaa atattgtaca 3306
aattttaata gcttaaattg tatatacagc caaataaaaaa cttgcattaa caaaaaaaaaa 3366
aaaaaaaaa 3374

```

```

<210> 2
<211> 617
<212> PRT
<213> Homo sapiens

<400> 2

```

```

Met Phe Arg Thr Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly
1           5           10          15

```

```

Ala Val Val Ala His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr
20           25          30

```

```

Val Val Tyr Leu Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile
35           40          45

```

```

Gln Ala Phe Val Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val
50           55          60

```

```

Phe Phe Gly Gln Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg
65           70          75          80

```

```

Ser Trp Tyr Ala Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg
85           90          95

```

```

Asp Asp Phe Ser Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Leu Phe
100          105         110

```

```

Leu Lys Cys Phe His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu
115          120         125

```

Arg Ser Pro Asn Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu
130 135 140

Met Phe Leu Leu Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr
145 150 155 160

His Ser Ile Leu Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe
165 170 175

Glu Tyr Ala Ile Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr
180 185 190

Val Leu His Ser Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys
195 200 205

Ala Val Tyr Met Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val
210 215 220

Leu Leu Tyr Met Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe
225 230 235 240

Pro Leu Phe Ala Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys
245 250 255

Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met
260 265 270

Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp
275 280 285

Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg
290 295 300

Leu Pro Cys Asn His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe
305 310 315 320

Gln Arg Gln Gln Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala
325 330 335

Ser Leu Pro Ala Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly
340 345 350

Pro Pro Pro Ala Pro His Pro Pro Pro Leu Leu Pro Gln Pro Pro Asn
 355 360 365

Phe Pro Gln Gly Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu
 370 375 380

Trp Pro Pro Met Gly Pro Phe Pro Pro Val Pro Pro Pro Pro Ser Ser
 385 390 395 400

Gly Glu Ala Val Ala Pro Pro Ser Thr Ser Ala Ala Ala Leu Ser Arg
 405 410 415

Pro Ser Gly Ala Ala Thr Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala
 420 425 430

Ala Ser Ala Thr Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala
 435 440 445

Gly Pro Ala Pro Gly Phe Pro Phe Pro Pro Pro Trp Met Gly Met Pro
 450 455 460

Leu Pro Pro Pro Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly
 465 470 475 480

Phe Ala Gly Leu Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu
 485 490 495

Arg Gln His Leu Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr
 500 505 510

Leu Leu Asp Ala Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu
 515 520 525

Ala Ser Leu Gly Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu
 530 535 540

Gly Thr Ala Thr Thr Val Val Ala Ala Ala Ser Ser Thr Ser Ile Pro
 545 550 555 560

Ser Ser Glu Ala Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro
 565 570 575

Glu Met Glu Arg Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met
580 585 590

Pro Glu Asp Gly Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu
595 600 605

Gln Lys Leu Glu Ser Pro Val Ala His
610 615

<210> 3
<211> 23
<212> DNA
<213> Homo sapiens

<400> 3
aatgtctgca tcattctgccg aga 23

<210> 4
<211> 23
<212> DNA
<213> Homo sapiens

<400> 4
aagctgtgac agatgccatc atg 23

<210> 5
<211> 23
<212> DNA
<213> Homo sapiens

<400> 5
aaagctgtga cagatgccat cat 23

<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
aagaaagctg tgacagatgc cat 23

<210> 7
<211> 23
<212> DNA
<213> Homo sapiens

<400> 7
aaggttctgc tgtacatggc ctt 23

<210> 8
<211> 23
<212> DNA
<213> Homo sapiens

<400> 8
aacaaggctg tgtacatgct cta 23

<210> 9
<211> 23
<212> DNA
<213> Homo sapiens

<400> 9
aaatgtttcc actggctggc tga 23

<210> 10
<211> 23
<212> DNA
<213> Homo sapiens

<400> 10
aaggtgttct ttgggcaact gag